

FIG. 1

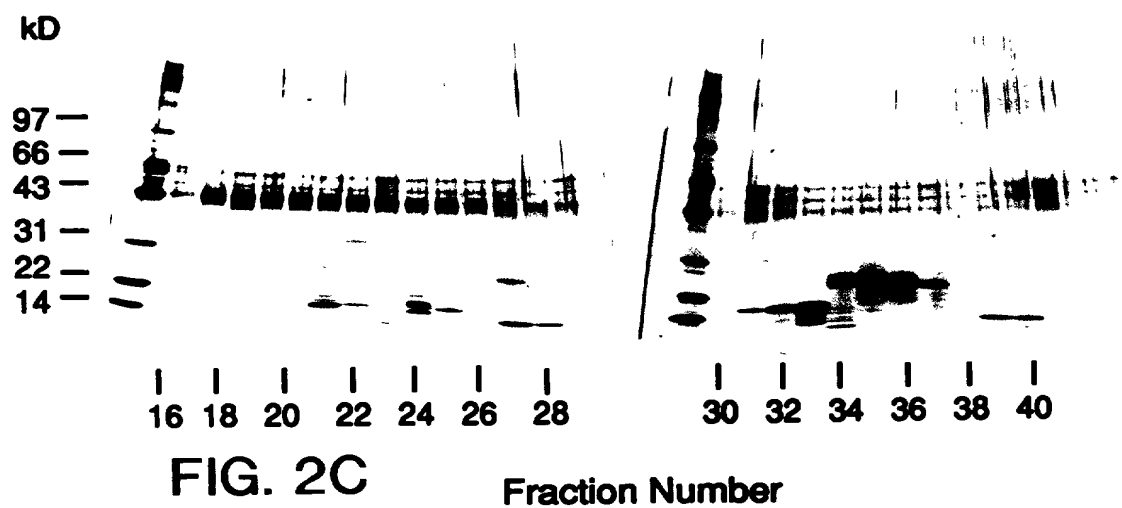
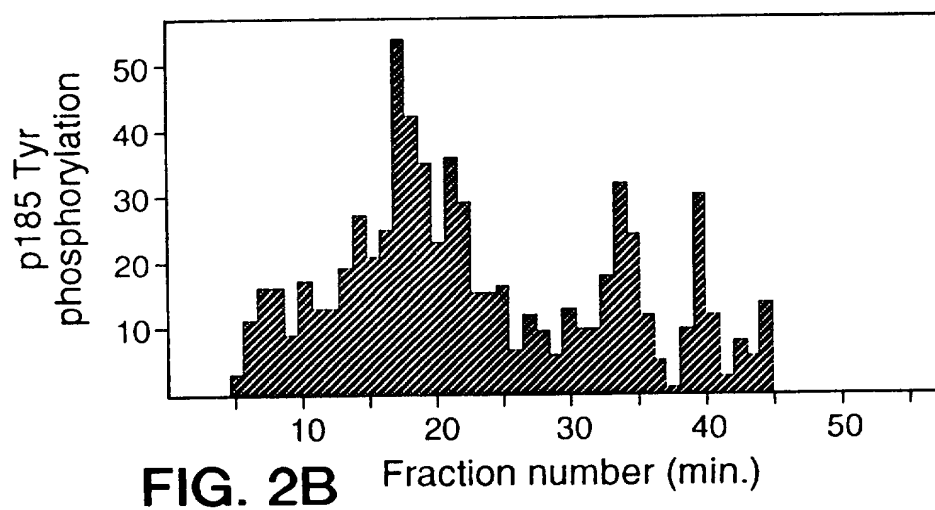
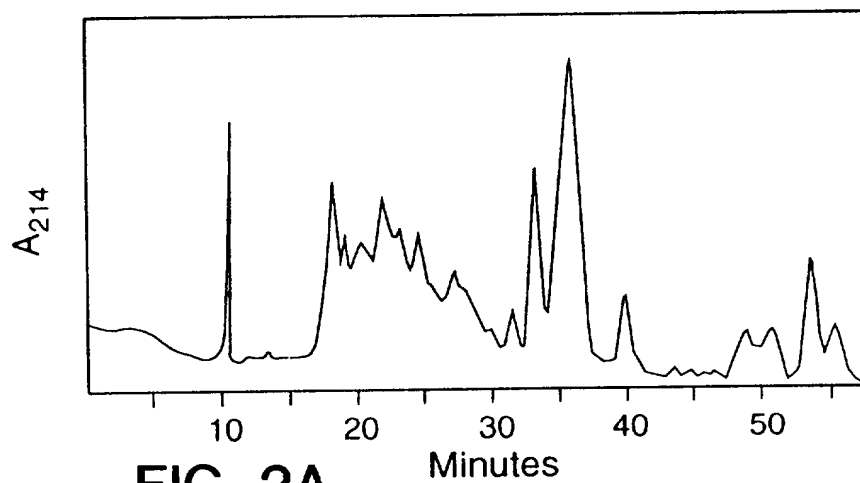


FIG. 3

GG	GCG	CGA	GCG	CCT	CAG	CGC	GGC	CGC	TCG	CTC	TCC	CCC	38
	Ala	Arg	Ala	Pro	Gln	Arg	Gly	Arg	Ser	Leu	Ser	Pro	
	1				5					10			
TCG	AGG	GAC	AAA	CTT	TTC	CCA	AAC	CCG	ATC	CGA	GCC	CTT	77
Ser	Arg	Asp	Lys	Leu	Phe	Pro	Asn	Pro	Ile	Arg	Ala	Leu	
		15					20					25	
GGA	CCA	AAC	TCG	CCT	GCG	CCG	AGA	GCC	GTC	CGC	GTA	GAG	116
Gly	Pro	Asn	Ser	Pro	Ala	Pro	Arg	Ala	Val	Arg	Val	Glu	
				30					35				
CGC	TCC	GTC	TCC	GGC	GAG	ATG	TCC	GAG	CGC	AAA	GAA	GGC	155
Arg	Ser	Val	Ser	Gly	Glu	Met	Ser	Glu	Arg	Lys	Glu	Gly	
	40					45					50		
AGA	GGC	AAA	GGG	AAG	GGC	AAG	AAG	AAG	GAG	CGA	GGC	TCC	194
Arg	Gly	Lys	Gly	Lys	Gly	Lys	Lys	Lys	Glu	Arg	Gly	Ser	
			55					60					
GGC	AAG	AAG	CCG	GAG	TCC	GCG	GCG	GGC	AGC	CAG	AGC	CCA	233
Gly	Lys	Lys	Pro	Glu	Ser	Ala	Ala	Gly	Ser	Gln	Ser	Pro	
	65				70					75			
GCC	TTG	CCT	CCC	CGA	TTG	AAA	GAG	ATG	AAA	AGC	CAG	GAA	272
Ala	Leu	Pro	Pro	Arg	Leu	Lys	Glu	Met	Lys	Ser	Gln	Glu	
		80					85					90	
TCG	GCT	GCA	GGT	TCC	AAA	CTA	GTC	CTT	CGG	TGT	GAA	ACC	311
Ser	Ala	Ala	Gly	Ser	Lys	Leu	Val	Leu	Arg	Cys	Glu	Thr	
				95					100				
AGT	TCT	GAA	TAC	TCC	TCT	CTC	AGA	TTC	AAG	TGG	TTC	AAG	350
Ser	Ser	Glu	Tyr	Ser	Ser	Leu	Arg	Phe	Lys	Trp	Phe	Lys	
	105					110					115		
AAT	GGG	AAT	GAA	TTG	AAT	CGA	AAA	AAC	AAA	CCA	CAA	AAT	389
Asn	Gly	Asn	Glu	Leu	Asn	Arg	Lys	Asn	Lys	Pro	Gln	Asn	
			120					125					
ATC	AAG	ATA	CAA	AAA	AAG	CCA	GGG	AAG	TCA	GAA	CTT	CGC	428
Ile	Lys	Ile	Gln	Lys	Lys	Pro	Gly	Lys	Ser	Glu	Leu	Arg	
					135					140			
ATT	AAC	AAA	GCA	TCA	CTG	GCT	GAT	TCT	GGA	GAG	TAT	ATG	467
Ile	Asn	Lys	Ala	Ser	Leu	Ala	Asp	Ser	Gly	Glu	Tyr	Met	
		145					150					155	
TGC	AAA	GTG	ATC	AGC	AAA	TTA	GGA	AAT	GAC	AGT	GCC	TCT	506
Cys	Lys	Val	Ile	Ser	Lys	Leu	Gly	Asn	Asp	Ser	Ala	Ser	
				160					165				

FIG. 4A

AAT GGG CCT CAC CAT CCT AAC CCA CCC CCC GAG AAT GTC 1052
 Asn Gly Pro His His Pro Asn Pro Pro Pro Glu Asn Val
 340 345 350

CAG CTG GTG AAT CAA TAC GTA TCT AAA AAC GTC ATC TCC 1091
 Gln Leu Val Asn Gln Tyr Val Ser Lys Asn Val Ile Ser
 355 360

AGT GAG CAT ATT GTT GAG AGA GAA GCA GAG ACA TCC TTT 1130
 Ser Glu His Ile Val Glu Arg Glu Ala Glu Thr Ser Phe
 365 370 375

TCC ACC AGT CAC TAT ACT TCC ACA GCC CAT CAC TCC ACT 1169
 Ser Thr Ser His Tyr Thr Ser Thr Ala His His Ser Thr
 380 385

ACT GTC ACC CAG ACT CCT AGC CAC AGC TGG AGC AAC GGA 1208
 Thr Val Thr Gln Thr Pro Ser His Ser Trp Ser Asn Gly
 390 395 400

CAC ACT GAA AGC ATC CTT TCC GAA AGC CAC TCT GTA ATC 1247
 His Thr Glu Ser Ile Leu Ser Glu Ser His Ser Val Ile
 405 410 415

GTG ATG TCA TCC GTA GAA AAC AGT AGG CAC AGC AGC CCA 1286
 Val Met Ser Ser Val Glu Asn Ser Arg His Ser Ser Pro
 420 425

ACT GGG GGC CCA AGA GGA CGT CTT AAT GGC ACA GGA GGC 1325
 Thr Gly Gly Pro Arg Gly Arg Leu Asn Gly Thr Gly Gly
 430 435 440

CCT CGT GAA TGT AAC AGC TTC CTC AGG CAT GCC AGA GAA 1364
 Pro Arg Glu Cys Asn Ser Phe Leu Arg His Ala Arg Glu
 445 450

ACC CCT GAT TCC TAC CGA GAC TCT CCT CAT AGT GAA AGG 1403
 Thr Pro Asp Ser Tyr Arg Asp Ser Pro His Ser Glu Arg
 455 460 465

TAT GTG TCA GCC ATG ACC ACC CCG GCT CGT ATG TCA CCT 1442
 Tyr Val Ser Ala Met Thr Thr Pro Ala Arg Met Ser Pro
 470 475 480

GTA GAT TTC CAC ACG CCA AGC TCC CCC AAA TCG CCC CCT 1481
 Val Asp Phe His Thr Pro Ser Ser Pro Lys Ser Pro Pro
 485 490

TCG GAA ATG TCT CCA CCC GTG TCC AGC ATG ACG GTG TCC 1520
 Ser Glu Met Ser Pro Pro Val Ser Ser Met Thr Val Ser
 495 500 505

FIG. 4C

ATG	CCT	TCC	ATG	GCG	GTC	AGC	CCC	TTC	ATG	GAA	GAA	GAG	1559
Met	Pro	Ser	Met	Ala	Val	Ser	Pro	Phe	Met	Glu	Glu	Glu	
			510					515					
AGA	CCT	CTA	CTT	CTC	GTG	ACA	CCA	CCA	AGG	CTG	CGG	GAG	1598
Arg	Pro	Leu	Leu	Leu	Val	Thr	Pro	Pro	Arg	Leu	Arg	Glu	
520					525					530			
AAG	AAG	TTT	GAC	CAT	CAC	CCT	CAG	CAG	TTC	AGC	TCC	TTC	1637
Lys	Lys	Phe	Asp	His	His	Pro	Gln	Gln	Phe	Ser	Ser	Phe	
		535					540					545	
CAC	CAC	AAC	CCC	GCG	CAT	GAC	AGT	AAC	AGC	CTC	CCT	GCT	1676
His	His	Asn	Pro	Ala	His	Asp	Ser	Asn	Ser	Leu	Pro	Ala	
				550					555				
AGC	CCC	TTG	AGG	ATA	GTG	GAG	GAT	GAG	GAG	TAT	GAA	ACG	1715
Ser	Pro	Leu	Arg	Ile	Val	Glu	Asp	Glu	Glu	Tyr	Glu	Thr	
	560					565					570		
ACC	CAA	GAG	TAC	GAG	CCA	GCC	CAA	GAG	CCT	GTT	AAG	AAA	1754
Thr	Gln	Glu	Tyr	Glu	Pro	Ala	Gln	Glu	Pro	Val	Lys	Lys	
			575					580					
CTC	GCC	AAT	AGC	CGG	CGG	GCC	AAA	AGA	ACC	AAG	CCC	AAT	1793
Leu	Ala	Asn	Ser	Arg	Arg	Ala	Lys	Arg	Thr	Lys	Pro	Asn	
585					590					595			
GGC	CAC	ATT	GCT	AAC	AGA	TTG	GAA	GTG	GAC	AGC	AAC	ACA	1832
Gly	His	Ile	Ala	Asn	Arg	Leu	Glu	Val	Asp	Ser	Asn	Thr	
		600					605					610	
AGC	TCC	CAG	AGC	AGT	AAC	TCA	GAG	AGT	GAA	ACA	GAA	GAT	1871
Ser	Ser	Gln	Ser	Ser	Asn	Ser	Glu	Ser	Glu	Thr	Glu	Asp	
				615					620				
GAA	AGA	GTA	GGT	GAA	GAT	ACG	CCT	TTC	CTG	GGC	ATA	CAG	1910
Glu	Arg	Val	Gly	Glu	Asp	Thr	Pro	Phe	Leu	Gly	Ile	Gln	
	625					630					635		
AAC	CCC	CTG	GCA	GCC	AGT	CTT	GAG	GCA	ACA	CCT	GCC	TTC	1949
Asn	Pro	Leu	Ala	Ala	Ser	Leu	Glu	Ala	Thr	Pro	Ala	Phe	
			640					645					
CGC	CTG	GCT	GAC	AGC	AGG	ACT	AAC	CCA	GCA	GGC	CGC	TTC	1988
Arg	Leu	Ala	Asp	Ser	Arg	Thr	Asn	Pro	Ala	Gly	Arg	Phe	
650					655					660			
TCG	ACA	CAG	GAA	GAA	ATC	CAG	G						2010
Ser	Thr	Gln	Glu	Glu	Ile	Gln							
		665				669							

FIG. 4D

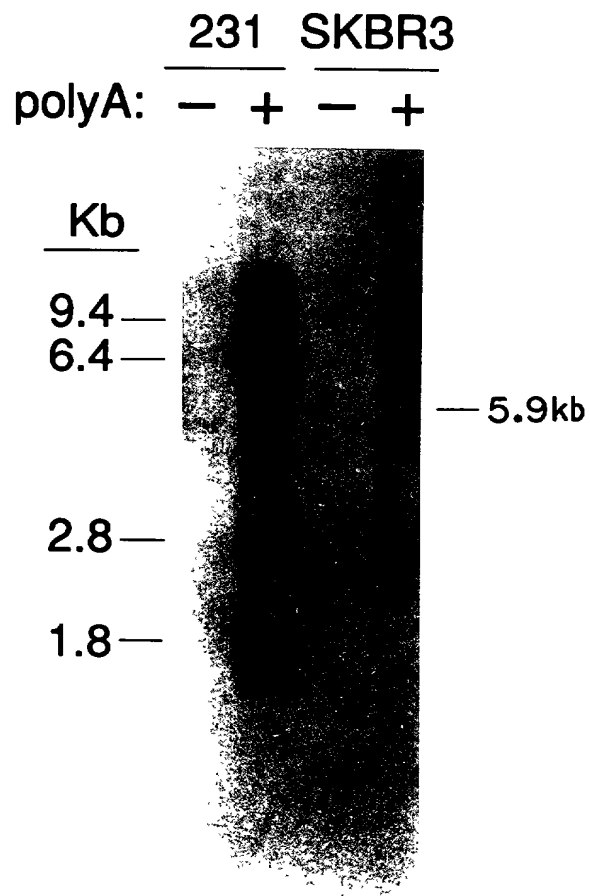
[illegible]

FIG. 5

HRG2-alpha	221	S	H	L	V	K	C	A	E	K	E	K	T	F	C	V	N	G	G	E	C	F	M	V	K	D	L	S	N	P	S	R	Y	L	C	K	C	Q	P	G	F	T	G	A	R	C	T	E	N
EGF		N	S	D	S	E	C	P	L	S	H	D	G	Y	C	L	H	D	G	V	C	M	Y	I	E	A	L	-	-	-	D	K	Y	A	C	N	C	V	V	G	Y	I	G	E	R	C	Q	Y	R
TGF-alpha																																																	
Amphiregulin																																																	
Schwannoma																																																	
HB-EGF																																																	

FIG. 7

HRG2-alpha	270	V	P	M	K	V	Q	N	Q	E	K	A	E	E	L	Y	Q	K	R	V	L	T	I	T	G	I	C	I	A	L	L	V	V	G	I	M	C	V	V	A	Y	C	K	T	K	K	Q	R	.	.
EGF		D	L	K	W	E	L	R	H	A	G	H	G	Q	Q	Q	Q	Q	Q	K	V	I	V	V	A	V	C	V	V	V	L	V	M	L	L	L	L	L	S	L	W	G	A	H	Y	Y	R	T	Q	K
TGF-alpha		D	L	L	A	V	V	A	S	Q	K	-	-	-	-	-	-	-	-	K	Q	A	I	T	A	L	V	V	S	I	V	A	L	A	V	L	I	I	T	C	V	L	I	H	C	C	Q	V		
Amphiregulin		S	M	K	T	H	S	M	I	D	S	S	L	S	-	-	-	-	-	K	I	A	L	A	I	A	A	F	M	S	A	V	I	L	T	A	V	A	V	I	T	V	Q	L	R	R	Q	Y		
Schwannoma		T	M	K	T	Q	K	K	D	D	S	D	L	S	-	-	-	-	-	K	I	A	L	A	A	I	I	V	F	V	S	A	V	S	V	A	A	I	G	I	I	T	A	V	L	L	R	K	R	
HB-EGF		S	L	P	V	E	N	R	L	Y	T	Y	D	-	-	-	-	-	-	H	T	T	I	L	A	V	V	A	V	V	L	S	S	V	C	L	L	V	I	V	G	L	L	M	F	R	Y	H	R	

TRANSMEMBRANE REGION

FIG. 6

HRG2-alpha	221	S	H	L	V	K	C	A	E	K	E	K	T	F	C	V	N	G	G	E	C	F	M	V	K	D	L	S	N	P	S	R	Y	L	C	K	C	Q	P	G	F	T	G	A	R	C	T	E	N		
EGF		N	S	D	S	E	C	P	L	S	H	D	G	Y	C	L	H	D	G	V	C	M	Y	I	E	A	L	-	-	-	D	K	Y	A	C	N	C	V	V	G	Y	I	G	E	R	C	Q	Y	R		
TGF-alpha							N	D	C	P	D	S	H	T	Q	F	C	F	H	-	G	T	C	R	F	L	V	Q	E	-	-	-	D	K	P	A	C	V	C	H	S	G	Y	V	G	A	R	C	E	H	A
Amphiregulin		K	K	K	N	P	C	N	A	E	F	Q	N	F	C	I	H	-	G	E	C	K	Y	I	E	H	L	-	-	-	E	A	V	T	C	K	C	Q	Q	E	Y	F	G	E	R	C	G	E	K		
Schwannoma		K	K	K	N	P	C	A	A	K	F	Q	N	F	C	I	H	-	G	E	C	R	Y	I	E	N	L	-	-	-	E	V	V	T	C	H	C	H	Q	D	Y	F	G	E	R	C	G	E	K		
HB-EGF		K	K	R	D	P	C	L	R	K	Y	K	D	F	C	I	H	-	G	E	C	K	Y	V	K	E	L	-	-	-	R	A	P	S	C	I	C	H	P	G	Y	H	G	E	R	C	H	G	L		
HRG2-alpha	270	V	P	M	K	V	Q	N	Q	E	K	A	E	E	L	Y	Q	K	R	V	L	T	I	T	G	I	C	I	A	L	L	V	V	G	I	M	C	V	V	A	Y	C	K	T	K	K	Q	R	.	.	
EGF		D	L	K	W	E	L	R	H	A	G	H	G	Q	Q	Q	-	K	V	I	V	V	A	V	C	V	V	L	V	M	L	L	L	L	L	L	S	L	W	G	A	H	Y	Y	R	T	Q	K			
TGF-alpha		D	L	L	A	V	V	A	A	S	Q	K	-	-	-	-	-	-	K	Q	A	I	T	A	L	V	V	S	I	V	A	L	A	V	L	I	I	T	C	V	L	I	H	C	C	Q	V				
Amphiregulin		S	M	K	T	H	S	M	I	D	S	S	L	S	-	-	-	-	K	I	A	L	A	I	A	A	F	M	S	A	V	I	L	T	A	V	A	V	I	T	V	Q	L	R	R	Q	Y				
Schwannoma		T	M	K	T	Q	K	K	D	D	S	D	L	S	-	-	-	-	K	I	A	L	A	I	I	V	F	V	S	A	V	S	V	A	A	I	G	I	I	T	A	V	L	L	R	K	R				
HB-EGF		S	L	P	V	E	N	R	L	Y	T	Y	D	-	-	-	-	-	H	T	T	I	L	A	V	V	A	V	V	L	S	S	V	C	L	L	V	I	V	G	L	L	M	F	R	Y	H	R			

TRANSMEMBRANE REGION

FIG 6

TRANSMEMBRANE REGION

FIG. 6

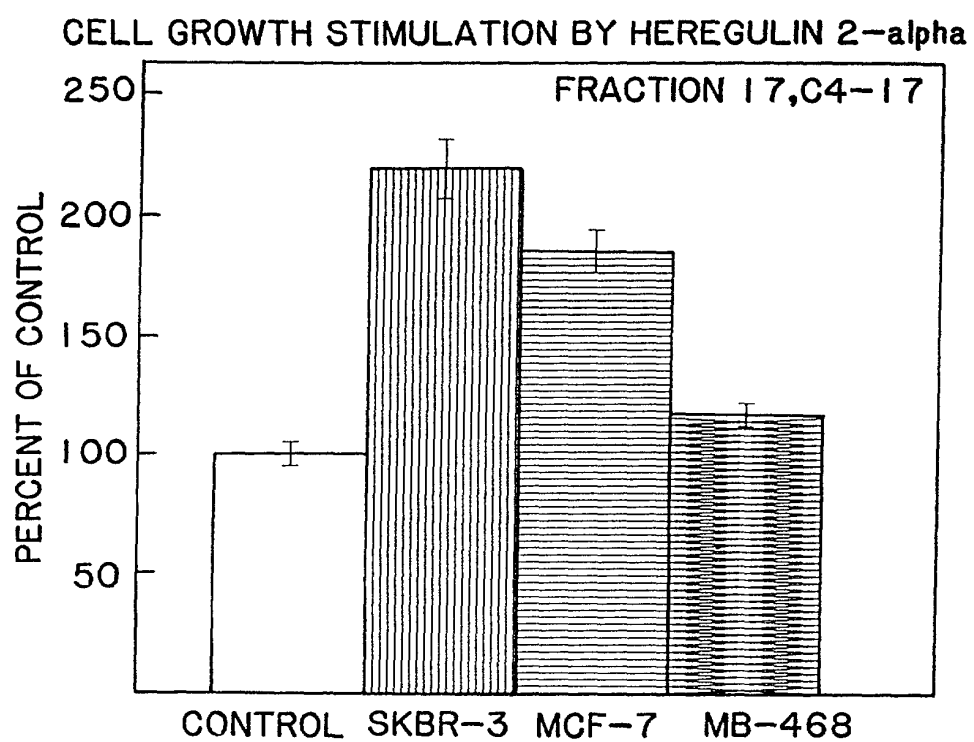


FIG. 7

(L) X R Q P K Y P R K S A P R R N K L D H Y A I I K F P L (T)
1 5 10 15 20 25

FIG. 8